

株日本触媒 基盤技術研究所 仙波 尚

Amino acid seq.
Cassava 由来 SHNL のアミノ酸配列(Gene Bank No. AJ223281)

MAVVDFVLIHTICHCAWIWYKLKPVLEAAGHKVTALDLAASGVDPRQIEQINSFDEYSEPLLTTFMESLPQ
GEKVILVGESCGGLNJAADKYPEKIAAAVFQNSLLPDTKIKPSYVVDKLMEVFPDWKDTEYFEFSNSN
GETITGMVLGLKLMRENLYTICPPEDYEAKMLTRRGSLFQSILAQREKFTEKGYGSIKKIYVWTGDDKI
FLPEFQLWQIENYKPDLVFKVMGGDIKKLQLTKTNEIAGILQKVADIYA

Amino acid seq.
Prunus 由来 RHNL のアミノ酸配列(Gene Bank No. AF043186)

MEKSTMSAVVLVLNLLVLJLQYSEVHSLANTSSEHDFGYLKFWNAV DLELECSYDYIIVGGGTSGCPLA
ATLSANYSVLVLERGTIATEYPNTLTVDCFAYNLQQQDDGKTPVERFVSEDGIDNVRSRILGGTTIINAGV
YARANESFYNNNSGVEWLDDLVNEAYEWVEDAIIVYKPSNQSWQSITGTAFLEAGVHPDNGFGLVHEEGT
RLTCSTFDNSGTRHASDEJJNKGDPDNLKVAVEAAVQKIIIFSTESSGLTAVGVVYTDNSNGTSRALVSGK
GEVILSAGTLGTPQLLLLSSGPESYLTSLNISVVA SHPYVCQYVNDNPRNFINILPPNPIEPSTVTLGITS
DFYQCSLSSLPDTPPFSLFPTTSYPLPNQTFAHTIVSKVPGPLSAGSLTLQSSSNVSAPNVKFNYCSDPV
DLTHCVSGMKKIGVFLSTDALKPYKVDDLPGIDGFNILGTPLPENQTDDAAFEKFCRDTVASYWHYHGG
AIVGKVIDGNFRVTGINALRVVDGSTFPATPASHPQGFYMLGRYVGTKIVQERSASGEAJHTSTFKPKLM
DSLKSALSFAF

両者のホモジニティ検索結果

[GENETYX : Maximum Matching]

Date : 2002.12.17

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Sequence 1 : M.esculenta SHNL AA seq

Size : 258

Matching Position : 1 - 258

Sequence 2 : P.serotina RHNL AA seq

Size : 574

Matching Position : 1 - 574

Matching Condition.

Matches : -1

Mismatches : 1

Gaps : 1

*N+ : 2

Matching : 15.68 [%]

Weight : 456

1 : M-----AVV -DFVL--IHT ICH----- --GAWIWYKL KPV----- LE-----
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1 : MEKSTMSAVV LVLNLVLHL QYSEVHSLAN TSSEHDFGYL KFVYNNAVDLE LEGSYDYIIV

28 : ----- AA ----- GHKVT ----- ALDLAASGVD PROIEQINSF
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61 : GGGTSGCPLA ATLSANYSVL VLERGTIA TE YPNTLTVDGF AYNLQQQDDG KTPVERFVSE

55 : D----EYSEP L----- ITFMESLP QGEKV---I LVGESCGGLN IAI-----
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121 : DGIDNVRSRI LGGTTIINAG VYARANESFY NNSGVEWLDL LVNEAYEWVE DAIVYKPSNQ

89 : ----- AADKYPEKI AAAV ----- FQNS ----- LL ----- PD -----
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181 : SWQSITGTAF LEAGVHPDNG FGLVHEEGTR LTGSTFDNSG TRHASDELLN KGDPDNLKVA

110 : -----TKHKP SYVVDKLMEV FPDWKD----- TEYF EFSNSNGETI TGMVLGL---
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241 : VEAAVQKIIIF STESSGLTAV GVVTDSNGT SHRALVSGKG EVILSAGTIG TPQLLLSGV

152 : -----KLMREN LYТИCPPEDY E-----
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301 : GPESYLTSLN ISVVASHPYV GQYVNDNPRN FINILPPNPI EPSTVTVLGI TSDFYQCSLS

169 : LAKMLTRRGS LF-----QS---IL AQREKF---
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361 : SLPFDTPPFS LFPTTSYPLP NQTFAHIVSK VPGPLSAGSL TIQSSSNVSV APNVKFNYCS

191 : -----TEKGY GSIK----- KIYV-- WTGDD--- KIFLPEFQ- -----
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421 : DPVDLTHCVS GMKKIGVFLS TDALKPYKVD DLPGIDGFNI LGTPLPENQT DDAAFEKPCR

217 : ----- LWQIENYKPD LVFRVMG--- ----- GDH KLQL----T
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481 : DTVASYWHYH GGAIVGKVID GNFRVTGINA LRVVDGSTFP ATPASHPQGF YLMLGRYVCT

242 : K-----TNEIAG IL---QKVAD IYA-
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541 : KIVQERSASG EAINTSTFKP KLMDSLKSAL SFAF

[GENETYX : Amino Acid Sequence Homology Data]

Date : 2002.12.17

1st Amino Acid Sequence

File Name : Cassava SHNL AA seq.
Sequence Size : 258

2nd Amino Acid Sequence

File Name : P.serotina RHNL AA seq
Sequence Size : 574

Unit Size to Compare = 2

Pick up Location = 1

[31.818% / 22 aa] INT/OPT.Score : < 21/ 63 >

1' MAVVDFVLIH TICHGAWIWy KLKPVLAAAG HKVTALDLAA SGVDPROIEQ INSFDEYSEP

1" MEKS TMSAVVLVLN LLVLHLQYSE

61' LLTFMESLPQ GEKVILVGES CGGLNIAIAA DKYPEKIAAA VFQNSLLPDT KHKPSYVVDK

25" VHSLANTSSE HDFGYLKFWY NAVDLELEGS YDYIIVGGGT SGCPLAATLS ANYSVLVLER

121' LMEVFPDWKD TEYFEFSNSN GETITGMVLG LKLMRENLYT ICPPEDYELA KMLTRRGSLF

85" GTIATEYPNT LTVDGFAYNL QQQDDGKTPV ERFVSEDGID NVRSRILGGT TIINAGVYAR

181' QSILAQREKF TEKGYGSIKK IYVWTGDDKI FLPEFQLWQI ENYKPDLVFR VMGGDHKLQL

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145" ANESFYNNNSG VEWDLDLVNE AYEWVEDAIV YKPSNQSWQS ITGTAFLLEAG VHPDNGFGLV

241' TKTNEIAGIL QKVADIYA

205" HEEGTRLTGS TFDNSGTRHA SDELLNKGD P DNLKVAVEAA VQKIIIFSTES SGLTAVGVVY